Table 1

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	21	1841446	COLNNOT07	869045R6 (LUNGAST01), 1251087F6 (LUNGFET03), 1574990F6 (LNODNOT03), 1841446H1 (COLNNOT07), 1860233F6 and 1860233T6 (PROSNOT18), 4999024H1 (MYEPTXT02)
2	22	1850310	LUNGFET03	045378H1 (CORNNOT01), 178670H1 (PLACNOB01), 1731750F6 (BRSTTUT08), 1850310F6 (LUNGFET03), 1850310H1, 1850310T6, and 1850465F6 (LUNGFET03), 2171482F6 (ENDCNOT03), 2771742H1 (COLANOT02), 3689884H1 (HE2ANOT01), 5388293H1 (BRAINOT19)
3	23	1887020	BLADTUT07	997447R1 (KIDNTUT01), 1603324F6 (LUNGNOT15), 1887020F6 and 1887020H1 (BLADTUT07), 3149213H1 (ADRENONN04), 3415447H1 (PTHYNOT04), 3472602H1 (LUNGNOT27), 5043722H2 (PLACFER01), 5300608H1 (MUSCNOT11)
4	24	1911421	CONNTUT01	276895H1 and 278868H1 (TESTNOT03), 1911421H1 and 1911421T6 (CONNTUT01), 2458650F6 (ENDANOT01)
5	25	1911910	CONNTUT01	1321511F1 (BLADNOT04), 1461469R1 (PANCNOT04), 1842277T6 (COLNNOT07), 1911910F6 and 1911910H1 (CONNTUT01)
6	26	1928920	BRSTNOT02	1928920H1 (BRSTNOT02), 637943F1 (BRSTNOT03), 1260702R1 (SYNORAT05), 1461588T1 (PANCNOT04), 1754346F6 (LIVRTUT01), 2906971F6 (THYMNOT05), 3368705F6 (CONNTUT04)
7	27	2170846	ENDCNOT03	2170846F6 and 2170846H1 (ENDCNOT03), 2828087T6 (TLYMNOT07), SBLA00670F1
8	28	2176361	ENDCNOT03	660127X30H2 (BRAINOT03), 1212293R6 (BRSTTUT01), 1310486T1 (COLNFET02), 1841413H1 (COLNNOT07), 2176361H1 and 2176361T6 (ENDCNOT03), 3212993T6 (BLADNOT08)
9	29	2212732	SINTFET03	285007F1 (LOSIHET02), 1002395R1 (BRSTNOT03), 2212732H1 (SINTFET03), 2361923R6 (LUNGFET05), 2708785T6 (PONSA2T01), 3605611H1 (LUNGNOT30)
10	30	2303457	BRSTNOT05	1573212F6 (LNODNOT03), 2303457H1 (BRSTNOT05), 2539058F6 (BONRTUT0), 3605342H1 (LUNGNOT30)

Table 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
11	31	2317552	OVARNOT02	409183F1 (EOSIHET02), 863694R1 and 863694T1 (BRAITUT03), 9136941 (STOMNOT02), 1319506T1 (BLADN\T04), 2317552H1 (OVARNOT02), 260410H1 (LUNGT\T07)
12	32	2416366	HNT3A2T01	220599F1 (PANCNOT01), 1384425T1 (BRAITUT08), 1636237F6 (UTRSNOT06), 241636H1 (HNT3A2T01), 260065F6 (UTRSNOT10), 286808F1F6 and 286808T1T6 (KIDNN\T20)
13	33	2472980	THP1NOT03	034079X6 and 034079T6 (THP1NOB01), 1595315F6 (BRAIN\T14), 2472980H1 (THP1NOT03), 2596942T6 (OVARTUT02), 385277T9T6 (BRAITUT12), 475486H1 (BRAHN\T01)
14	34	2541640	BONRTUT01	621985F1 and 621985R6 (PGANNOT01), 2541640F6 and 254164H1 (BONRTUT01), 5314848H1 (KIDETXS02)
15	35	2695204	UTRSNOT12	927986N1 (BRAINOT04), 18541076 (HNT3A2T01), 269520H1 (UTRSNOT12), 3464157F6 (293IF2T01), 359682\H1 (F1BPNOT01)
16	36	2805526	BLADTUT08	161563F1 (ADENINB01), 1275596F6 (TESTTUT02), 1508327F6 (LUNGNOT14), 1965858H1 (BRSTNOT04), 220790IF6 (SINTFET03), 2805526H1 (BLADTUT08), 360295\F6 (DRGTNOT01)
17	37	2850382	BRSTTUT13	1217874T1 (NEUTCMOT01), 1267183F1 (BRAINOT09), 1515874F1 (PANCTUT01), 2234171F6 (PANCTUT02), 2850382H1 (BRSTTUT13), 308501\4H1 (HEAQNOT03)
18	38	2929276	TLYMNOT04	2929276H1 (TLYMNOT04) 13645R1 (SYNORAB01), 149704R1 (FIBRN\T02), 123182\8X27 (BRAITUT01), 123614\4F1 (LUNGN\T03), 1351889F1 (LATRTUT02), 1381121F1 (BRAITUT08), 2509933F6 (CONUTUT01), 281941\2H1 (BRSTN\T14), 3029720H1 (HEARFET02), 497855H1 (OVARDIT01)

Table 1 (cont.)

Protein SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
19	39	3033039	TLYMNOT05	3033039H1 (TLYMNOT05), 1235556F1 and 1251391F1 (LUNGFET03), 1261615H1 (SYNORAT05), 1413023F6 (BRAINOT12), 1425681T1 (BEPINON01), 1498538F1 (SINTBST01), 1562136F1 (SPLNNOT04), 1901480T6 (BLADTUT06), 2170485F6 (ENDCNOT03), 2454842P6 (ENDANOT01), 2915250H1 (THYMFET03), 4248873H1 (BRADDIR01), 4721266H1 (BRAIHCT02), 4939383H1 (BRAIFEN03), 5094946H1 (EPIMNON05), 5151444H1 (HEARFET03)
20	40	3039890	BRSTNOT16	1535201T1 (SPLNNOT04), 1576892T1 (LNODNOT03), 2517426H1 (BRAITUT21), 2715705H1 (THYRNOT09), 3039890H1 and 3039890T6 (BRSTNOT16), SBMA03391F1, SBMA028^2F1, SBMA02370F1

Table 2

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites
1	349	S53 T114 T147 S11 S15 S141 S149 T156 S225 T252 S299 T313 T342 S343	N250
2	169	T39 T88 T71 S119 T128	N126
3	316	T85 S194 T196 S80 T230	
4	220	T39 S10 T169 S77 S205 S208	N15
5	235	S13 T153 S128 S182 S134 T187 Y155	
6	407	S235 S3 S183 T149	
7	212	S59 T84 Y147	L448
8	241	T167 S168 S48 T79 S129 S7 T36 S66 T86 T219	N57 N206
9	375	T67 T11 S123 S132 T317 S8 S81 T173 S355 Y19	
10	429	S257 S40 T90 S117 S232 S234 S236 T242 S2 T242 T252 S256 S387	N88 N173 N283
11	329	S8 T10 S29 S47 S49 S57 S227 S260 S314 T86 S124 S277	N64 N114 N122 N250
12	476	S195 T246 T453 S459 S10 S20 S22 S34 S55 S57 S72 S77 S95 S97 S118 S122 S137 S168 S184 S211 T263 S330 T357 T392 S415 S443 S64 S83 S86 S106 S197 T308 T382 S431 T437 S438	N3 N376
13	366	S330 T119 T188 S60 T65 S140 S185 T298 S305 T326 T337 S344 S357	N39 N161 N202 N269 N273 N348 N352
14	152	T81 T148 S45	N28
15	233	T87 S18 T172 S186 S189 S203	
16	357	T118 S189 T62 T80 S115 T126 S247 S273 S328 S337	N130
17	251	T48 T224 S106 T114 S126 S161 S180 T202 S235	
18	105	S49 T69 T98 S15 S34	
19	876	S119 S179 T180 S226 T262 T386 S450 S494 S529 T542 S560 S585 T689 S716 T728 S770 S804 T35 T110 T123 S238 T248 T457 S574 S634 S693 T702 S733 S745 S806	N397 N644
20	505	S377 S4 T129 S179 T338 T339 T413 T484 S179 S208 S377 S439 S463 S474 S491	N320 N477

Table 3

Nucleotide SEQ ID NO:	Useful Fragment	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
21	596-640	Reproductive (0.235) Hematopoietic/Immune (0.148) Cardiovascular (0.136)	Cancer (0.432) Inflammation (0.284) Cell Proliferation (0.222)	pSPORT1
22	1380-1424	Reproductive (0.296) Nervous (0.167) Gastrointestinal (0.130)	Cancer (0.426) Inflammation (0.222) Cell Proliferation (0.204)	pINCY
23	273-317	Reproductive (0.200) Cardiovascular (0.175) Nervous (0.175)	Cancer (0.475) Cell Proliferation (0.175) Inflammation (0.175)	pINCY
24	111-155	Reproductive (0.215) Cardiovascular (0.139) Nervous (0.139)	Cancer (0.430) Inflammation (0.241) Cell Proliferation (0.228)	pINCY
25	217-261	Nervous (0.351) Gastrointestinal (0.135) Reproductive (0.135)	Cancer (0.405) Cell Proliferation (0.216) Inflammation (0.189)	pINCY
26	543-587	Reproductive (0.237) Gastrointestinal (0.175) Nervous (0.150)	Cancer (0.475) Inflammation (0.237) Cell Proliferation (0.225)	pSPORT1
27	138-182	Reproductive (0.250) Cardiovascular (0.200) Gastrointestinal (0.150)	Cancer (0.500) Cell Proliferation (0.250)	pINCY
28	1029-1073	Reproductive (0.325) Nervous (0.125) Urologic (0.125)	Cancer (0.450) Cell Proliferation (0.200) Inflammation (0.150)	pINCY
29	434-478	Nervous (0.250) Reproductive (0.222) Gastrointestinal (0.139)	Cancer (0.444) Inflammation (0.306) Cell Proliferation (0.194)	pINCY
30	327-372	Reproductive (0.333) Nervous (0.278) Cardiovascular (0.111)	Cancer (0.389) Inflammation (0.278) Cell Proliferation (0.111)	pSPORT1
31	992-1036	Nervous (0.235) Reproductive (0.235) Gastrointestinal (0.157)	Cancer (0.382) Inflammation (0.255) Cell Proliferation (0.235)	pSPORT1

Table 3 (cont.)

Nucleotide SEQ ID NO:	Useful Fragment	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
32	325-369	Nervous (0.250) Reproductive (0.219) Hematopoietic/Immune (0.172)	Cancer (0.484) Inflammation (0.203) Cell Proliferation (0.141)	pINCY
33	336-380	Reproductive (0.219) Developmental (0.156) Hematopoietic/Immune (0.156)	Cancer (0.438) Inflammation (0.250) Cell Proliferation (0.219)	pINCY
34	109-153	Reproductive (0.364) Gastrointestinal (0.273) Musculoskeletal (0.182)	Cancer (0.818) Cell Proliferation (0.091) Trauma (0.091)	pINCY
35	597-641	Nervous (0.211) Reproductive (0.211) Hematopoietic/Immune (0.132)	Cancer (0.395) Inflammation (0.263) Cell Proliferation (0.132)	pINCY
36	921-965	Reproductive (0.324) Nervous (0.135) Developmental (0.108)	Cancer (0.514) Inflammation (0.162) Cell Proliferation (0.135)	pINCY
37	381-425	Reproductive (0.269) Nervous (0.192) Hematopoietic/Immune (0.141)	Cancer (0.436) Inflammation (0.192) Cell Proliferation (0.167)	pINCY
38	109-153	Reproductive (0.281) Hematopoietic/Immune (0.132) Cardiovascular (0.114)	Cancer (0.412) Inflammation (0.333) Cell Proliferation (0.158)	pINCY
39	433-477	Nervous (0.206) Reproductive (0.206) Cardiovascular (0.150)	Cancer (0.477) Cell Proliferation (0.224) Inflammation (0.206)	pINCY
40	596-640	Reproductive (0.239) Nervous (0.181) Hematopoietic/Immune (0.129)	Cancer (0.439) Inflammation (0.219) Cell Proliferation (0.194)	pINCY

Table 4

Nucleotide SEQ ID NO:	Library	Library Comment
21	COLNNOT07	Library was constructed using RNA isolated from colon tissue removed from a 60-year-old Caucasian male during a left hemicolectomy.
22	LUNGFET03	Library was constructed using RNA isolated from lung tissue removed from a Caucasian female fetus, who died at 20 weeks' gestation.
23	BLADTUT07	Library was constructed using RNA isolated from bladder tumor tissue removed from the anterior bladder wall of a 58-year-old Caucasian male during a radical cystectomy, radical prostatectomy, and gastrostomy. Pathology indicated a grade 3 transitional cell carcinoma in the left lateral bladder. Patient history included angina and emphysema. Family history included acute myocardial infarction, atherosclerotic coronary artery disease, and type II diabetes.
24	CONNTUT01	Library was constructed using RNA isolated from a soft tissue tumor removed from the clival area of the skull of a 30-year-old Caucasian female. Pathology indicated chondroid chordoma with neoplastic cells reactive for keratin.
25	CONNTUT01	Library was constructed using RNA isolated from a soft tissue tumor removed from the clival area of the skull of a 30-year-old Caucasian female. Pathology indicated chondroid chordoma with neoplastic cells reactive for keratin.
26	BRSTNOT02	Library was constructed using RNA isolated from diseased breast tissue removed from a 55-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated proliferative fibrocysytic changes characterized by apocrine metaplasia, sclerosing adenosis, cyst formation, and ductal hyperplasia without atypia. Pathology for the associated tumor tissue indicated an invasive grade 4 mammary adenocarcinoma. Patient history included atrial tachycardia and a benign neoplasm. Family history included cardiovascular and cerebrovascular disease.
27	ENDCNOT03	Library was constructed using RNA isolated from dermal microvascular endothelial cells removed from a neonatal Caucasian male.
28	ENDCNOT03	Library was constructed using RNA isolated from dermal microvascular endothelial cells removed from a neonatal Caucasian male.
29	SINTFET03	Library was constructed using RNA isolated from small intestine tissue removed from a Caucasian female fetus, who died at 20 weeks' gestation.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
30	BRSTNOT05	Library was constructed using RNA isolated from breast tissue removed from a 58-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated multicentric invasive grade 4 lobular carcinoma. Patient history included skin cancer, rheumatic heart disease, osteoarthritis, and tuberculosis. Family history included cerebrovascular and cardiovascular disease, breast and prostate cancer, and type I diabetes.
31	OVARNOT02	Library was constructed using RNA isolated from ovarian tissue removed from a 59-year-old Caucasian female who died of a myocardial infarction. Patient history included cardiomyopathy, coronary artery disease, previous myocardial infarctions, hypercholesterolemia, hypertension, and arthritis.
32	HNT3AZT01	Library was constructed using RNA isolated from the hNT2 cell line (derived from a human teratocarcinoma that exhibited properties characteristic of a committed neuronal precursor). Cells were treated for three days with 0.35 micromolar 5-aza-2'-deoxycytidine (A2).
33	THP1NOT03	Library was constructed using polyA RNA isolated from untreated THP-1 cells. THP-1 (ATCC TIB 202) is a human promonocyte line derived from the peripheral blood of a 1-year-old Caucasian male with acute monocytic leukemia (ref: Int. J. Cancer (1980) 26:171).
34	BONRTUT01	Library was constructed using RNA isolated from rib tumor tissue removed from a 16-year-old Caucasian male during a rib osteotomy and a wedge resection of the lung. Pathology indicated a metastatic grade 3 (of 4) osteosarcoma, forming a mass involving the chest wall.
35	UTRSNOT12	Library was constructed using RNA isolated from uterine myometrial tissue removed from a 41-year-old Caucasian female during a vaginal hysterectomy with dilation and curettage. The endometrium was secretory and contained fragments of endometrial polyps. Benign endo- and ectocervical mucosa were identified in the endocervix. Pathology for the associated tumor tissue indicated uterine leiomyoma.
36	BLADTUT08	Library was constructed using RNA isolated from bladder tumor tissue removed from a 72-year-old Caucasian male during a radical cystectomy and prostatectomy. Pathology indicated an invasive grade 3 (of 3) transitional cell carcinoma in the right bladder base. Family history included myocardial infarction, cerebrovascular disease, and brain cancer.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
37	BRSTTUT13	Library was constructed using RNA isolated from breast tumor tissue removed from the right breast of a 46-year-old Caucasian female during a unilateral extended simple mastectomy with breast reconstruction. Pathology indicated an invasive grade 3 adenocarcinoma, ductal type with apocrine features and greater than 50% intraductal component. Patient history included breast cancer.
38	TLYMNOT04	Library was constructed using 0.5 micrograms of polyA RNA isolated from activated Th1 cells. These cells were differentiated from umbilical cord CD4 T cells with IL-12 and B7-transfected COS cells, and then activated for six hours with anti-CD3 and anti-CD28 antibodies.
39	TLYMNOT05	Library was constructed using polyA RNA isolated from nonactivated Th2 cells. These cells were differentiated from umbilical cord CD4 T cells with IL-4 in the presence of anti-IL-12 antibodies and B7-transfected COS cells.
40	BRSTNOT16	Library was constructed using RNA isolated from diseased breast tissue removed from the right breast of a 59-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated papillomatosis. Pathology for the associated tumor tissue indicated an invasive lobular carcinoma with extension into ducts, forming an ill-defined mass situated in the biopsy cavity site. Multiple axillary lymph nodes were negative for tumor. Prior right breast biopsy indicated invasive grade 3, nuclear grade 3, invasive and in situ ductal carcinoma. Estrogen and progesterone immunostains were positive in the neoplastic cells. Patient history included liver cirrhosis, esophageal ulcer, hyperlipidemia, and neuropathy.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.	*ESTs*: Probability value= 1.0E-8 or less *Full Length sequences*: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, tfasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad Sci. 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489.	*ESTs*: fasta E value=1.06E-6 *Assembled ESTs*: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less *Full Length sequences*: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS and PRINTS databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S and J.G. Henikoff, Nucl. Acid Res., 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37: 417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and Probability value= 1.0E-3 or less
PFAM	A Hidden Markov Models-based application useful for protein family search.	Krogh, A. et al. (1994) J. Mol. Biol., 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits, depending on individual protein families

Table 5 cont.

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25: 217-221.	Score= 4.0 or greater
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M. S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12: 431-439.	Score=5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch et al. supra; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	